SEQUENCE LISTING

<110> VIVIER, ERIC
MORETTA, ALESSANDRO
OLCESE, LUCIA
VELY, FREDERIC
TOMASELLO, ELENA

<120> NEW POLYPEPTIDES ASSOCIATED WITH ACTIVATORY RECEPTORS AND THEIR BIOLOGICAL APPLICATIONS

OIPE JC109 JUL 26 2002 PATENT & TRADEMARK OFFICE

<130> 1721-18

<140> 09/403,980
<141> 2000-01-19

<150> PCT/FR98/00883
<151> 1998-04-30

<150> FR 97/05411
<151> 1997-04-30

<150> FR 98/00927
<151> 1998-01-28

<160> 44

<170> PatentIn Ver. 2.1

<210> 1
<211> 517
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (138)..(398)

<400> 1
ggtcacacca ggtcccacca gcccctggac tgtggtgtcc agtgcatatc tggccaccat 60

ggggctctgg agcctcctgg tgccttctgt tccttcctgt cctcctgact gtgggaggat 120

taagtcccgt acaggcc cag agt gac act ttc cca aga tgc gac tgt tct 170
Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser
1 5 10

tcc gtg agc cct ggt gta ctg tct ggg att gtt ctg ggt gac ttg gtg 218
Ser Val Ser Pro Gly Val Leu Ser Gly Ile Val Leu Gly Asp Leu Val
15 20 25

ttg act ctg ctg att gcc ctg gct gtg tac tct ctg ggc cgc ctg gtc 266
Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val
30 35 40

tcc cga ggt caa ggg aca gcg gaa ggg acc cgg aaa caa cac att gct 314
Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala

45 50 55

gag act gag tcg cct tat cag gag ctt cag ggt cag aga cat gaa gta 362
Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val
60 65 70 75

tac agt gac ctc aac aca cag agg caa tat tac aga tgagcccact 408
Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg
80 85

ctatgcccat cagcggcctg atgcccggat ccggtcattc cagatgccta ctcaacaagc 468

cctctctgag atcaggactc ccgttggaat acagatccac agggtacct 517

<210> 2
<211> 87
<212> PRT
<213> Mus musculus

<400> 2
Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly
1 5 10 15

Val Leu Ser Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile
20 25 30

Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly
35 40 45

Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro
50 55 60

Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn
65 70 75 80

Thr Gln Arg Gln Tyr Tyr Arg
85

<210> 3
<211> 16
<212> PRT
<213> Mus musculus

<400> 3
Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly
1 5 10 15

<210> 4
<211> 24
<212> PRT
<213> Mus musculus

<400> 4
Val Leu Ser Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile

1 5 10 15

Ala Leu Ala Val Tyr Ser Leu Gly
20

<210> 5
<211> 47
<212> PRT
<213> Mus musculus

<400> 5
Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln
1 5 10 15

His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
20 25 30

His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg
35 40 45

<210> 6
<211> 515
<212> DNA
<213> Mus musculus

<400> 6
tcacaccagg tcccaccagc ccctggactg tggtgtccag tgcatatctg gccaccatgg 60
ggctctggag cctcctggtg ccttctgttc cttcctgtcc tcctgactgt gggaggatta 120
agtcccgtac aggcccagag tgacactttc ccaagatgcg actgttcttc cgtgagccct 180
ggtgtactgt ctgggattgt tctgggtgac ttggtgttga ctctgctgat tgccctggct 240
gtgtactctc tgggccgcct ggtctcccga ggtcaaggga cagcggaagg gacccggaaa 300
caacacattg ctgagactga gtcgccttat caggagcttc agggtcagag acatgaagta 360
tacagtgacc tcaacacaca gaggcaatat tacagatgag cccactctat gcccatcagc 420
ggcctgatgc ccggatccgg tcattccaga tgcctactca acaagccctc tctgagatca 480
ggactcccgt tggaatacag atccacaggg tacct 515

<210> 7
<211> 371
<212> DNA
<213> Mus musculus

<400> 7
gtgcatatct ggccaccatg ggggctctgg agcctccatg gtgccttctg ttccttcctg 60
tcctcctgac tgtgggagga ttaagtcccg tacaggccca gagtgacact ttcccaagat 120
gcgactgttc ttccgtgagc cctggtgtac tggctgggat tgttctgggt gacttggtgt 180
tgactctgct gattgccctg gctgtgtact ctctcggccg cctggtctcc cgaggtcaag 240
ggacagcgga agggacccgg aaacaacaca ttgctgagac tgagtcgcct tatcaggagc 300
ttcagggtca gagaccagaa gtatacagtg acctcaacac acagaggcaa tattacagat 360
gagcccactc t 371

<210> 8
<211> 376
<212> DNA

<213> Mus musculus

<400> 8
gccttctgtt ccttcctgtc ctcctgactg tgggaggatt aagtcccgta caggcccaga 60
gtgacacttt cccaagatgc ggctgttctt ccgtgagccc tggtgtactg gctgggattg 120
ttctgggtga cttggtgttg actctgctga ttgccctggc tgtgtactct ctgggccgcc 180
tggtctcccg aggtcaaggg acagcggaag ggacccggaa acaacacatt gctgagactg 240
agtcgcctta tcaggagctt cagggtcaga gacatgaagt atacagtgac ctcaacacac 300
agaggcaata ttacagatga gcccactcta tgcccatcag cggcctgatg cccggatccg 360
gtcattccag atgcct 376

<210> 9
<211> 402
<212> DNA
<213> Mus musculus

<400> 9
ccagcccctg gactgtggtg tccagtgcat atctggccac catgggggct ctggagcctc 60
ctggtgcctt ctgttccttc ctgtcctcct gactgtggga ggattaagtc ccgtacaggc 120
ccagagtgac actttcccaa gatgcgactg ttcttccgtg agccctggtg tactggctgg 180
gattgttctg ggtgacttgg tgttgactct gctgattgcc ctggctgtgt actctctggg 240
ccgcctggtc tcccgaggtc aagggacagc ggaagggacc cggaaacaac acattgctga 300
gactgagtcg ccttatcagg agcttcaggg tcagagacca gaagtataca gtgacctcaa 360
cacacagagg caatattaca gatgagccac tctatgccca tc 402

<210> 10
<211> 482
<212> DNA
<213> Mus musculus

<400> 10
gttccttcct gtcctcctga ctgtgggagg attaagtccc gtacaggccc agagtgacac 60
tttcccaaga tgcgactgtt cttccgtgag ccctggtgta ctggctggga ttgttctggg 120
tgacttggtg ttgactctgc tgattgccct ggctgtgtac tctctgggcc gcctggtctc 180
ccgaggtcaa gggacagcgg aagggacccg gaaacaacac attgctgaga ctgagtcgcc 240
ttatcaggag cttcagggtc agagacctga agtatacagt gacctcaaca cacagaggcg 300
atattacaga tgagcccact ctatgcccat cagcggcctg atgcccggat ccggtcattc 360
cagatgccta ctcaacaagc ccttctgtgg gatcaggact cccgttggaa tacagatcca 420
cagggtacct ccctgagata tctgacattg taccatttct gtccccaaat agaagacgga 480
ca 482

<210> 11
<211> 171
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (133)
<223> Any amino acid

<400> 11
Ser His Gln Val Pro Pro Ala Pro Gly Leu Trp Cys Pro Val His Ile
1 5 10 15

Trp Pro Pro Trp Gly Ser Gly Ala Ser Trp Cys Leu Leu Phe Leu Pro
20 25 30

Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp
35 40 45

Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ser
50 55 60

Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala
65 70 75 80

Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu
85 90 95

Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu
100 105 110

Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg
115 120 125

Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile Ser Gly Leu Met Pro
130 135 140

Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Ser Leu Arg Ser
145 150 155 160

Gly Leu Pro Leu Glu Tyr Arg Ser Thr Gly Tyr
165 170

<210> 12
<211> 123
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (120)
<223> Any amino acid

<400> 12
Ala Tyr Leu Ala Thr Met Gly Ala Leu Glu Pro Pro Trp Cys Leu Leu
1 5 10 15

Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala
20 25 30

Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly
35 40 45

Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile
50 55 60

Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly
65 70 75 80

Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro
85 90 95

Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn
100 105 110

Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser
115 120

<210> 13
<211> 124
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (106)
<223> Any amino acid

<400> 13
Leu Leu Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val
1 5 10 15

Gln Ala Gln Ser Asp Thr Phe Pro Arg Cys Gly Cys Ser Ser Val Ser
20 25 30

Pro Gly Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu
35 40 45

Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly
50 55 60

Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu
65 70 75 80

Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp
85 90 95

Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile
100 105 110

Ser Gly Leu Met Pro Gly Ser Gly His Ser Arg Cys
115 120

<210> 14
<211> 133
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (128)
<223> Any amino acid

<400> 14
Gln Pro Leu Asp Cys Gly Val Gln Cys Ile Ser Gly His His Gly Gly
1 5 10 15

Ser Gly Ala Ser Trp Cys Leu Leu Phe Leu Pro Val Leu Leu Thr Val
20 25 30

Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe Pro Arg Cys
35 40 45

Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile Val Leu Gly
50 55 60

Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly
65 70 75 80

Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln
85 90 95

His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
100 105 110

Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa
115 120 125

Ala Thr Leu Cys Pro
130

<210> 15
<211> 160
<212> PRT
<213> Mus musculus

<220>
<221> MOD_RES
<222> (104)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (145)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (148)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (157)

<400> 15
Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala
1 5 10 15

Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly
20 25 30

Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile
35 40 45

Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly
50 55 60

Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro
65 70 75 80

Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn
85 90 95

Thr Gln Arg Arg Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile Ser Gly
100 105 110

Leu Met Pro Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Phe
115 120 125

Cys Gly Ile Arg Thr Pro Val Gly Ile Gln Ile His Arg Val Pro Pro
130 135 140

Xaa Asp Ile Xaa His Cys Thr Ile Ser Val Pro Lys Xaa Lys Thr Asp
145 150 155 160

<210> 16
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 16
tcacaccagg tcccaccagc ccctggactg tggtgtccag tgcatatctg gccaccatgg 60
gggctctgga gcctccatgg tgccttctgt tccttcctgt cctcctgact gtgggaggat 120
taagtcccgt acaggcccag agtgacactt tcccaagatg cgrctgttct tccgtgagcc 180
ctggtgtact gkctgggatt gttctgggtg acttggtgtt gactctgctg attgccctgg 240
ctgtgtactc tctsggccgc ctggtctccc gaggtcaagg gacagcggaa gggacccgga 300
aacaacacat tgctgagact gagtcgcctt atcaggagct tcagggtcag agacmwgaag 360
tatacagtga cctcaacaca cagaggcrat attacagatg agcccactct atgcccatca 420
gcggcctgat gcccggatcc ggtcattcca gatgcctact caacaagccc ttctstgrga 480
tcaggactcc cgttggaata cagatccaca gggtacctcc ctgagatatc tgacattgta 540
ccatttctgt ccccaaatag aagacggaca 570

<210> 17
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus

sequence

<220>
<221> MOD_RES
<222> (108)
<223> Any amino acid

<400> 17
Trp Cys Leu Leu Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser
1 5 10 15

Pro Val Gln Ala Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser
20 25 30

Val Ser Pro Gly Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu
35 40 45

Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser
50 55 60

Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu
65 70 75 80

Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr
85 90 95

Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser Met
100 105 110

Pro Ile Ser Gly Leu Met Pro Gly Ser Gly His Ser Arg Cys
115 120 125

<210> 18
<211> 2838
<212> DNA
<213> Mus musculus

<400> 18
acaccaggtc ccaccagccc ctggactgtg gtgtccagtg catatctggc caccatgggg 60
gctctggagc cctcctggtg ccttctgttc cttcctgtcc tcctgactgt gtaggtgagt 120
cgggggggctt ctgtggatgc ctcctgtgtc ctcagctcat gttggggcca ggactaggca 180
gagagcagga agggacagca cagacaaggg gaaggctggg cagaagaagg ttcctctaga 240
gcctgtgggt ttcaccctga gctagaggcc ctgagatttg gaacctggta gtatcagtag 300
gggggacatt gaagctcaca gatataccta ccacatgttg gtcagtaccg gccgctgggt 360
gctgtgagac cagctctttc caaccttctt caccttctac atccactgtc tgtgcctcaa 420
tttacatctt tcttttgaat atagaatcac atatagccca ggctagcttc aaatttgcta 480
cgtaattgag gataacctca acctttctat tctctgtctc cacctctctc agtttacctg 540
ttctttttctc cttaggatta agtcccgtac aggcccagag tggtaagcca taatacccccc 600
gatctttctc tcttcctctc aaagacctcc tcaggccacc ccttctcctt ctagccctct 660
ttgtgctaac accaagccct gattgttaac ctgtgtcccc ctcttcatcc tcctgagaca 720
ctttcccaag atgcgactgt tcttccgtga gccctggtgt actggctggg attgttctgg 780
gtgacttggt gttgactctg ctgattgccc tggctgtgta ctctctgggc cgcctggtct 840
cccgaggtca agagagtaag aaggtaaata aatctttaaa aaaaattgtc ccagtcccca 900
gcttagtcct tcttcacacc atatgtcact ctctatccct ctctagggac ccggaaacaa 960
cacattgctg agactgagtc gccttatcag gtaagaacgc caaattcttc tccacccttg 1020
ctcctgcccc gtcctggcta tccccctccc cagtacagac acacagacaa acacacacac 1080

acaaatacac agagacatat ataaacacac tcacataaat aaacacacac acatacctac 1140
acacacacac acacatacct acacacacac acacacatac ctacacacac acacacacac 1200
acacacacac actacccttc ccagaacctt aaggtccctt cctcaggagc tcccccaatc 1260
ctgaaggcaa aggactaact gtcaaacata ttcggtggtc aaccatgacc tttaagctca 1320
gcttctaatg agtctcttgt caagattcta ttcctctgtc tctctctctc tctctctctc 1380
tctctctctc tctctctctc tctctctctc tctgcgtgtg tgtgtgtgtg tgtgtgtgtg 1440
tgtgtaggca ggttataaga ggacatcaaa tcctatcttt accttatttt taaaatggca 1500
ctgattttgc tctgtattta catgtgtgtg tggagcaggt gtgcatatgc actggcagcc 1560
atgtgggggt cagaagacaa cccgtggggg ctggttctct ccttccacct tgtggatctc 1620
tgaactctaa attctagttg tcaagcttgg cagcaagtgc tttacccact gaaccatctc 1680
accagcccca agcctccttc ctaacctttg ggctctgggt gaggctatgt ctctagggaa 1740
acacacacca ggctggtctc tggtacatgc tctcagagac tctgcccctg ggaggcacag 1800
acccctgctc tgtgacccaa tttctggaag tctacctccc tccctgtagc cagttttgcc 1860
cattcgactg actccttgct ggaggaactt tttctctgaa aagtgttaga atctcttgat 1920
tcttgttttg agtttggtgt ggggaagtag tggcgtgtgt ctttaatccc agcgctctgg 1980
tggcagaggt aggcagatct ctgtgaattt gaggctggcc tggtctacag tgtgagttcc 2040
tggacaggca gggctaccca aagaaaccct gtctacaagc aaacaaacaa acaaaaacaa 2100
aacaaaacaa aaaagaatct caatattggc catctgatgt ccagaagacc ccgggctgtc 2160
tagtttctga gagccaggaa actttagggc aaatgtcagc ctgatttttt tatccttcgg 2220
tatcttggtt gaggcctaca tggatcaaca cagcactcca attggagaag cttatttgaa 2280
gcaacttaac aaaatcattt ggggtgacat tatgaagaga ttgaagtgaa ccaatataat 2340
ggtgggacag gaaagaaact gaagatgggg aaactaaaac attgccaaga ctcaaagggt 2400
gagcaggttg aagatctgtg ggcttggtgc tccaggcatc ggggtggggg gctgcacatg 2460
taaggaccct ggggttggtg cctaatgtgc aggcagaaag gccaggagaa tgctgagtgc 2520
atttgaataa aatcttgacc ttttcatgat tttaagtttg aaaaacctgc cagagacctt 2580
gaaggtcatt aggaggctag atttgttttt atttgctggg ccccctccaa tgatggcctt 2640
ttttttttt tttaaggagc ttcagggtca gagaccagaa gtatacagtg acctcaacac 2700
acagaggcaa tattacagat gagcccactc tatgcccatc agcggcctga tgcccggatc 2760
cggtcattcc agatgcctac tcaacaagcc ctctctgaga tcaggactcc cgttggaata 2820
cagatccaca gggtacct 2838

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
ggctctggag ccctcctggt gc 22

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
actctgggcc tgtacgggac t 21

<210> 21

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
agtcccgtac aggcccagag t 21

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
cagagtcaac accaagtcac c 21

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
ggtgacttgg tgttgactct g 21

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ctcagtctca gcaatgtgtt g 21

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
caacacattg ctgagactga g 21

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26 21
ctgtgtgttg aggtcactgt a

<210> 27
<211> 452
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(333)

<400> 27
atg ggg gct ctg gag ccc tcc tgg tgc ctt ctg ttc ctt cct gtc ctc 48
Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu
1 5 10 15

ctg act gtg gag gga tta agt ccc gta cag gcc cag agt gac act ttc 96
Leu Thr Val Glu Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe
20 25 30

cca aga tgc gac tgt tct tcc gtg agc cct ggt gta ctg gct ggg att 144
Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile
35 40 45

gtt ctg ggt gac ttg gtg ttg act ctg ctg att gcc ctg gct gtg tac 192
Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr
50 55 60

tct ctg ggc cgc ctg gtc tcc cga ggt caa gag agg acc cgg aaa caa 240
Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln
65 70 75 80

cac att gct gag act gag tcg cct tat cag gag ctt cag ggt cag aga 288
His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
85 90 95

cat gaa gta tac agt gac ctc aac aca cag agg caa tat tac aga 333
His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg
100 105 110

tgagcccact ctatgcccat cagcggcctg atgcccggat ccggtcattc cagatgccta 393

ctcaacaagc cctctctgag atcaggactc ccgttggaat acagatccac agggtacct 452

<210> 28
<211> 111
<212> PRT
<213> Mus musculus

<400> 28
Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu
1 5 10 15

Leu Thr Val Glu Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe
20 25 30

Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile
35 40 45

Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr
50 55 60

Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln
65 70 75 80

His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
85 90 95

His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg
100 105 110

<210> 29
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
ccgctcgagg gcttcatggg gggacttgaa c 31

<210> 30
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
ctagtctaga ggatccaggt atcattgtgc tgactgtcat gattcg 46

<210> 31
<211> 431
<212> DNA
<213> Mus musculus

<400> 31
ggcttcgttt tctgttctgc gccgttacag atccaagctc ctcgagggct tcatgggggg 60
acttgaaccc tgcagcaggc tcctgctcct gcctctcctg ctggctgtaa gtggtctccg 120
tcctgtccag gcccaggccc agagcgattg cagttgctct acggtgagcc cgggcgtgct 180
ggcagggatc gtgatgggag acctggtgct gacagtgctc attgccctgg ccgtgtactt 240
cctgggccgg ctggtccctc gggggcgagg ggctgcggag gcagcgaccc ggaaacagcg 300
tatcactgag accgagtcgc cttatcagga gctccagggt cagaggtcgg atgtctacag 360
cgacctcaac acacagaggc cgtattacaa atgagcccga atcatgacag tcagcacaat 420
gatacctgga t 431

<210> 32
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 32
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
1 5 10 15

<210> 33
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 33
Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
1 5 10 15

<210> 34
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 34
Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
1 5 10 15

<210> 35
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 35
Tyr Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu
1 5 10 15

<210> 36
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 36
Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr Ser His Leu
1 5 10 15

<210> 37
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 37
Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu
1 5 10 15

<210> 38
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 38
Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly Thr Tyr Gln Asp Val
1 5 10 15

<210> 39
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 39
Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile
1 5 10 15

<210> 40
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 40
Tyr Thr Gly Leu Asp Thr Arg Asn Gln Glu Thr Tyr Glu Thr Leu
1 5 10 15

<210> 41
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 41
Tyr Glu Glu Leu Asn Ile Tyr Ser Ala Thr Tyr Ser Glu Leu
1 5 10

<210> 42
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 42
Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu
1 5 10 15

<210> 43
<211> 109
<212> PRT
<213> Mus musculus

<400> 43

Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu
1 5 10 15

Leu Thr Val Leu Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe
20 25 30

Pro Arg Cys Asp Cys Ser Ser Val Pro Gly Val Leu Ala Gly Ile Val
35 40 45

Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Tyr Ser Leu
50 55 60

Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln His Ile
65 70 75 80

Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu
85 90 95

Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg
100 105

<210> 44
<211> 111
<212> PRT
<213> Mus musculus

<400> 44
Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu
1 5 10 15

Leu Thr Val Glu Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe
20 25 30

Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile
35 40 45

Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Ile
50 55 60

Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln
65 70 75 80

His Ile Ala Arg Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
85 90 95

Pro Glu Val Tyr Ser Asp Leu Arg Thr Gln Arg Gln Tyr Tyr Arg
100 105 110